AMENDMENTS TO THE CLAIMS

Listing of Claims:

1. (Original) A recombination system comprising:

a transgenic recombination construct capable of being inserted into the chromosomal DNA of a eukaryotic organism said construct comprising in a 5'- to 3'-orientation;

a first homology sequence A and at least one recognition sequence for site-directed induction of DNA double-strand breaks; and

a second homology sequence B,

wherein the homology sequences A and B have a sufficient length and a sufficient homology that allows for homologous recombination; and

an enzyme suitable for inducing DNA double-strand breaks at a recognition sequence for the site-directed induction of DNA double-strand breaks or a nucleic acid sequence encoding said enzyme.

2. (Original) The system of claim 1, wherein the construct, after said first homology sequence, contains a further nucleic acid sequence.

3. (Original) The system of claim 2, wherein the construct further contains a second recognition sequence for the site-directed induction of DNA double-strand breaks.

4. (Currently amended) The system of claim 2, wherein the further nucleic acid sequence contains at least one of the elements selected from the group consisting of ~~positive selection markers, negative~~ selection markers, reporter genes, replication origins, multiple cloning regions, border sequences for Agrobacterium transfection, sequences which enable homologous recombination or insertion into a genome of a host organism, expression cassette for an enzyme suitable for inducing DNA double-strand breaks at the recognition sequence for the site-directed induction of DNA double-strand breaks and combinations thereof.

5. (Currently amended) The system of claim 1, wherein the construct further contains at least one of the elements selected from the group consisting of ~~positive selection markers, negative~~ selection markers, reporter genes, replication origins, multiple cloning regions, border sequences for Agrobacterium transfection, sequences which enable homologous recombination or insertion into a genome of a host organism, expression cassette for an enzyme suitable for inducing DNA double-strand breaks at the recognition sequence for the site-directed induction of DNA double-strand breaks and combinations thereof.

6. (Original) The system of claim 1, wherein the enzyme is selected from the group consisting of restriction endonucleases, homing endonucleases, group II intron endonucleases, recombinases, transposases, chimeric nucleases and combinations thereof.

7. (Original) The system of claim 1, wherein the enzyme is selected from the group consisting of F-SceI, F-SceII, F-SuvI, F-TevI, F-TevII, I-AmaI, I-AniI, I-CeuI, I-CeuAIIP, I-ChuI, I-CmoeI, I-CpaI, I-CpaII, I-CreI, I-CrepsbIP, I-CrepsbIIP, I-CrepsbIIIP, I-CrepsbIVP, I-CsmI, I-CvuI, I-CvuAIP, I-DdiI, I-DdiII, I-DirI, I-DmoI, I-HmuI, I-HmuII, I-HspNIP, I-LlaI, I-MsoI, I-NaaI, I-NanI, I-Nc1IP, I-NgrIP, I-NitI, I-NjaI, I-Nsp236IP, I-PakI, I-PboIP, I-PcuIP, I-PcuAI, I-PcuVI, I-PgrIP, I-PobIP, I-PorI, I-PorIIP, I-PpbIP, I-PpoI, I-SPBetaIP, I-ScaI, I-SceI, I-SceII, I-SceIII, I-SceIV, I-SceV, I-SceVI, I-SceVII, I-SexIP, I-SneIP, I-SpomCP, I-SpomIP, I-SpomIIP, I-SquIP, I-Ssp6803I, I-SthPhiJP, I-SthPhiST3P, I-SthPhiS3bP, I-TdeIP, I-TevI, I-TevII, I-TevIII, I-UarAP, I-UarHGPA1P, I-UarHGPA13P, I-VinIP, I-ZbiIP, PI-MtuI, PI-MtuHIP, PI-MtuHIIP, PI-PfuI, PI-PfuII, PI-PkoI, PI-PkoII, PI-PspI, PI-Rma43812IP, PI-SPBetaIP, PI-SceI, PI-TfuI, PI-TfuII, PI-ThyI, PI-TliI, PI-TliII and combinations thereof.

8. (Original) The system of claim 1, wherein the enzyme is selected from the group consisting of enzymes encoded by the sequence as shown in SEQ ID NO: 2, 4, 6, 8 or 10, and combinations thereof.

9. (Original) The system of claim 1, wherein the enzyme is expressed from an expression cassette that contains a nucleic acid sequence encoding said enzyme.

10. (Original) The system of claim 9, wherein the nucleic acid sequence encoding said enzyme comprises the sequence as shown in SEQ ID NO: 1, 3, 5, 7 or 9.

11. (Currently amended) A method for removing a DNA sequence from chromosomal DNA of a eukaryotic cell or organism comprising:

combining a transgenic recombination construct inserted into the chromosomal DNA of a eukaryotic cell or organism, said construct comprising, in a 5' - to 3' -orientation, a first homology sequence A and at least one recognition sequence for the site-directed induction of DNA double-strand breaks; and a second homology sequence B, wherein the homology sequences A and B have a sufficient length and a sufficient homology that allows for homologous recombination; with an enzyme suitable for inducing DNA double-strand breaks at a recognition sequence for the site-directed induction of DNA double-strand breaks;

inducing DNA double-strand breaks at the recognition sequence; and

conducting homologous recombination between the homology sequences A and B.

12. (Original) The method of claim 11, wherein the construct contains a further nucleic acid sequence.

13. (Currently amended) The method of claim 12, wherein the further nucleic acid sequence contains at least one of the elements selected from the group consisting of ~~positive selection markers, negative~~ selection markers, reporter genes, replication origins, multiple cloning regions, border sequences for Agrobacterium transfection, sequences which enable homologous recombination or insertion into a genome of a host organism, expression cassette for an enzyme suitable for inducing DNA double-strand breaks at the recognition sequence for the site-directed induction of DNA double-strand breaks and combinations thereof.

14. The method of claim 11, wherein the construct, after said first homology sequence A contains a second recognition sequence for the site-directed induction of DNA double-strand breaks.

15. (Currently amended) The method of claim 11, wherein the construct contains at least one of the elements selected from the group consisting of ~~positive selection markers, negative~~ selection markers, reporter genes, replication origins, multiple cloning regions, border sequences for Agrobacterium transfection, sequences which enable homologous recombination or insertion into a genome of a host organism, expression cassette for an enzyme suitable for inducing DNA double-strand breaks at the recognition sequence for the site-directed induction of DNA double-strand breaks and combinations thereof.

16. (Original) The method of claim 11, wherein the enzyme is selected from the group consisting of restriction endonucleases, homing endonucleases, recombinases, transposases, chimeric nucleases and combinations thereof.

17. (Original) The method of claim 11, wherein the enzyme is selected from the group consisting of F-SceI, F-SCeII, F-SuvI, F-TevI, F-TevII, I-AmaI, I-AniI, I-CeuI, I-CeuAIIP, I-ChuI, I-CmoeI, I-CpaI, I-CpaII, I-CreI, I-CrepsbIP, I-CrepsbIIP, I-CrepsbIIIP, I-CrepsbIVP, I-CsmI, I-CvuI, I-CvuAIP, I-DdiI, I-DdiII, I-DirI, I-DmoI, I-HmuI, I-HmuII, I-HspNIP, I-LlaI, I-MsoI, I-NaaI, I-NanI, I-Nc1IP, I-NgrIP, I-NitI, I-NjaI, I-Nsp236IP, I-PakI, I-PboIP, I-PcuIP, I-PcuAI, I-PcuVI, I-PgrIP, I-PobIP, I-PorI, I-PorIIP, I-PpbIP, I-PpoI, I-SPBetaIP, I-ScaI, I-SceI, I-SceII, I-SceIII, I-SceIV, I-SceV, I-SceVI, I-SceVII, I-SexIP, I-SneIP, I-SpomCP, I-SpomIP, I-SpomIIP, I-SquIP, I-Ssp6803I, I-SthPhiJP, I-SthPhiST3P, I-SthPhiS3bP, I-TdeIP, I-TevI, I-TevII, I-TevIII, I-UarAP, I-UarHGPA1P, I-UarHGPA13P, I-VinIP, I-ZbiIP, PI-MtuI, PI-MtuHIP, PI-MtuHIIP, PI-PfuI, PI-PfuII, PI-PkoI, PI-PkoII, PI-PspI, PI-Rma43812IP, PI-SPBetaIP, PI-SceI, PI-TfuI, PI-TfuII, PI-ThyI, PI-TliI, PI-TliII and combinations thereof.

18. (Original) The method of claim 11, wherein the enzyme is selected from the group consisting of enzymes that contain the sequence as shown in SEQ ID NO: 2, 4, 6, 8 or 10, and combinations thereof.

19. (Original) The method of claim 11, wherein the enzyme is encoded in an expression cassette.

20. (Original) The method of claim 11, wherein the nucleic acid sequence comprises the sequence as shown in SEQ ID NO: 1, 3, 5, 7 or 9, or a combination thereof.

21. (Original) An organism comprising the recombination system of claim 1.

22. (Original) The organism of claim 21 selected from the group consisting of yeasts, algae, fungi and animal and plant organisms.

23. (Original) The organism of claim 21 which is a plant organism.

24. (Original) The organism of claim 22, wherein the plant organism is selected from the group consisting of Arabidopsis thaliana, tobacco, wheat, rye, barley, oats, oilseed rape, maize, potato, sugar beet, soybean, sunflower, pumpkin/squash and peanut.

25. (Original) A cell culture, organ, tissue, part or transgenic propagation material derived from the organism of claim 21.

26. (Original) A method for the production of foodstuff, feedstuff, seeds, pharmaceuticals or fine chemicals comprising expressing said foodstuff, feedstuff, seeds, pharmaceuticals or fine chemicals from the recombinant system of the organism of claim 20.

27. (New) The system of claim 2, wherein the further nucleic acid sequence comprises an expression cassette for an enzyme suitable for inducing DNA double-strand breaks at the recognition sequence for the site-directed induction of DNA double-strand breaks.

28. (New) The system of claim 1, wherein the construct further comprises an expression cassette for an enzyme suitable for inducing DNA double-strand breaks at the recognition sequence for the site-directed induction of DNA double-strand breaks.

29. (New) The method of claim 12, wherein the further nucleic acid sequence comprises an expression cassette for an enzyme suitable for inducing DNA double-strand breaks at the recognition sequence for the site-directed induction of DNA double-strand breaks.

30. (New) The method of claim 11, wherein the construct comprises an expression cassette for an enzyme suitable for inducing DNA double-strand breaks at the recognition sequence for the site-directed induction of DNA double-strand breaks.